FOR OFFICIAL	USE ONLY

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00-	Scientific and I	Technical Info	rmation Center	r		
CNE	SEARCH	REQUES	ST FORM			
Requester's Full Name: Art Unit: 1635 Location (Bldg/Room#): 25 ***********************************	TERRA GIBBS Phone Number: 2- 0 (Mailbox #): 20 ***********************************	758 18 Result	Serial Number Format Preferr	ed (circle): PA	J37 PER DI	SK
To ensure an efficient and quality	emsen, please attach a cop			,,	•.	ME
Title of Invention:	· · · · · · · · · · · · · · · · · · ·				1	<u> </u>
Inventors (please provide full	names):				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
F	* ***			,	<u> </u>	
Earliest Priority Date: Search Topic:		·	•			3 :
Please provide a detailed statement elected species or structures, keywo Define any terms that may have a strong Sequence Searches Only* Plappropriate serial number.	ords, synonyms, acronyms,	nd registry numbers ples or relevant cita formation (parent, d	s, and combine with tions, authors, etc., i	the concept or util f known. ssued patent numb	ity of the invo	ention. ith the
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83% identity	•	·		<i>[50</i>	arb 013 22:518	njen
I need th	e Same Corrisoris	on with	ar vegulti	of 90/ i	identit	y
with SEa J	Dyo: 5 (ma	leo boses	1715-206	o) as Exh	ubit B	Shows

2. I also need the Same comparison with a result of 93% identity with SED TO Mail MA - 3358 - 2 His is confusing)

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Terra,

Seg! has 100% local similarity with "Query!".

Seg! is much longer than Query!, so the overall query

match is low & can't be improved significantly.

I tried 8 different sets of parameter changes (altering Gap penalty 8 for Gap size penalty) to get the best match between Seg 2, nt 1715 - 5066 vs Query 1. The best I could a come up with was 82.5% Best Local Similarity (green tab).

Please let me know if you have questions.

Barb

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ALIGNMENTS

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                                                                                                        8; Gaps
                                                                     Query Match 57.3%; Score 198.2; DB 1; Length 337; Best Local Similarity 80.8%; Pred. No. 0; Matches 277; Conservative 0; Mismatches 58; Indels 8
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85 TGGCCCTCTCACATTCCTGATTCACATATTCAGAGGGTTAGCTTGTCCTCC 140 Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels (RESULT 2
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Search completed: May 25, 2005, 16:32:24 Job time : 1 secs

294 IGGAGCCCTCCACCAGCCCGTIATATATAGCTAGGGCTGAGATAATCTTCC 239

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Compugen Ltd.
GenCore version (c) 1993 - 2005
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nucleic search, using sw model OM nucleic

// Search time 0.872041 Seconds
(without alignments)
1.822 Million cell updates/sec May 25, 2005, 16:34:51 ü

Run

US-10-005-337A-1-COPY 2358

Title: Perfect score:

.....caggtcggaggccaccatgg 2358 1 ggatcctttcatgtttaaca Sequence:

IDENTITY NUC Gapop 10.0 Scoring table:

1 segs, 337 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed . 08 08 Minimum Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

new.seg:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Entered (bobryen Entered (bobryen Description QUERY 1 Π - -DB 337 Query Match Length 14.3 Score 337 4 6 Š

ALIGNMENTS

QUERY 1 ; Entered [bobryen 25-May-05 16:13] QUERY 1

Gaps . 0 Length 337; 0; Indels DB 1; Query Match

14.3%; Score 337; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG

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ņ. 1091 AGTGAGGAGAGACAGATATATGATGGCCAGCATAACAAAACATACACAACACCCCTAATTAA 1150 1331 CTCAACAGCAAAGCTTGGGGCCTTTTTGTTTCCGTGTTAGGAATAGAACACGAGAGCCCC 1390 971 AAGGTATTAGTGTTTGGTTTTCAGGGCAATGTCTTGTACTGAAGATTCTAGAAACACAA 1030 1031 TTTGCTGGTTGAACAGCTGAAGTGGGGTGGGGGTTCTTACCCCATGTTCATGGAAGGGTG 1090 151 CACTTCCCTCTTCTACTGACACCCCCTTCACTCTCCTCTTTCATAAAAAATAAAAAGT 1210 1211 ATTTTATGTGGCTCTTACGATAGAATCTTTCCTCGAACTATAAAAAGATCTAAATATTTA 1270 1330 610 670 790 241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGGTGTGGAGGGCTCCACAGGGC 300 266 671 AGATCCTTGGCCTTGAATTAGGGAGGCACAAAATACTCAGAGATTCAAGACTGCTC 730 197 850 ------AATTCAGAGGCAGGTGAATTTTCATTCCAGACTTAGTGTCTCGGAAGCC 148 ---- 131 911 ATAGCGTCTCAGGACAGATAGGACAGAGAGAACACTAGGAGAGGGGAACCCACGAAGGAC 970 --- 101 611 CTCTGCATCCATAGCAAGTAGCCTAATGTTTCTGTGTCTAGGTGTCATCTCTGTGAATCG 731 AGCAGCCCAGAGTCCTTCCTCAAAGGAAAGGTCTCAACTCTCAGCCCCCTTAGCTCTGA -----TCCAGCCTGGGAAGCCAAGTCACACCCCTGCCCCCACCAGTGGCC---TCTTATGGGTGGAGCCAAGACGCATCGTGGGTGGAGCGAAGACGCAACCTCACCTTCTAG 325 retrieredatedadecerregaactegecereredadeceerecacacacacacatratar CAAGAGGTCAAAGAAAATAGTGTTAACCATGAAAAACGAGAAGACCAACAGTTATCCATTG 791 GTCAGGCCTGGAACAAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTGCTTGTCACTT 1271 TATTTTTCACATTTTAATATCTTAGCGATGACAAGCCAGAAACAAGTATTTTTGCCTCT Gaps Indels 1186; Length 337; CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308 0.9%; Score ... 0; 10.8%; Pred. No. 0; ... 0; Migmatches 151; 265 AGCTAGGGCTGGGTGAGATATCT----RESULT 2 QUERY 1/c ; Entered [bobryen 25-May-05 16:13] QUERY_1 Best Local Similarity 10.8 Matches 162; Conservative 2272 301 851 130 130 130 551 196 130 241 241 130 130 130 Query Match 셤 ò 셤 ઠે g ò 셤 ઠે 셤 ઠ 요 ઠે 셤 8 셤 ò g ઠે g ઠે a ઠે g ઠે a ò g è 유 ઠે g

Maximum Match 100% Listing first 45 summaries	Database : new.seq:*	No. is the number of results predigreater than or equal to the score	s derived by analysis of the total score distribut STMWARTES	* Query	Score Match Length DB ID Description 202.2 58.4 337 1 QUERY 1 Entered	5 4.3 337 1. QUERY_1	ALIGNMENTS	RESULT 1 QUERY 1 ; Entered [bobryen 25-May-05 16:13]	tch 58.4%; Score 202.2; DB 1; Length 337; al Similarity 80.8%; Pred. No. 0;	Matches 27/; Conservative 0; Mismatches 58; Indels 8; Gaps 4;	1 GCAATATAACAGGCAGCTGCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG	Qy 60 AGCGATGTGATCACCACCAAGGAATGGCCCTCTCACATTTCTTCCTGATTTCACATATTC 119	61 AGUGGIGIGGICACIGCCAAAGGAAIGACCICICACAIIICIICCIGAIICGCAIACGC	Oy 120 AGCAGGGTTAGCTCCCCCCCCTCTTCAGCTTCCCAGACACTGAGTCTGGAATGA 179	176 AAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGAGGTGTGACTTGGCTTCCCAG	Qy 240 GTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGCCCAG 299	Db 236 GCTGGAAGATTATCTCACCCTAGCTATATAA-CGGGCTGGTGGAGGGGCTCCA 294 Ov 300 CAGGGCAACTCCAGGATTCCTTC-CACGACAAAAACATA 341		RESULT 2 QUERY 1/c		cch 4.3%; Score 15; DB 1; Length 337; al Similarity 26.7%; Pred. No. 0;	Matches 62	BS 103CCTCTCACATTCTTCTCACAAATTACAAAATTACAAAATTACAAAATTACAAAAATCTTCCCTCATAAAAAA	145 CTCTTCAGCTTCCCAGACACTGGAATGAAAATTCACCTGCCTCTGAGTTGGCT	238	Qy 205 CCTAATGGGGGGGGGGGGGTGTTCGGTTGGAAGATTATCTCACCGGCCC 264
1391 GTGTATCTAGGCAGATGCTCTATCATTAGCCCATGAGTCTCCAGGCCTCAGACGCACATTT	100	Db 100 101	Qy 1511 TTGTGCTTCTGCTAAGAACTGGACTCACATCTCTGTGCATCACTTCGGCCCGTTTTGG 1570	100	QY 1571 GGTAGATCCTCTGATTAGCTTTAGAACACGGTGAGCCTGTGGTGACTTA 1630 Db 100 101	1631 TGGCCAGTGACATAGAGTCAAAGTGCATTACTGAATGCTTTCAATTTCTCCTAATGC	Db 100 101	Oy 1691 TGGTACGATGGCATGTCACAGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAA 1750 Db	63	Qy 1811 AAATAGGATGTCCCAAAGCAACATTCCCAGCCAACTGGAGTGCTGATAAGATGTTAT 1870	1871 CAGAAAGATATGGCTGTAAGTGTGATGCACAGTGCTTGCATTTTCTTGATACGTTAGTCA	(5)	1931 TATGAGAGCTGACAAAGAAAAAAGAGCAGCGATGTGGGCAATATTAACAGGCAGCT	Db . 63 64 Qy 1991 GTCCCCTGGCTTCCGATAGGTGGGATGGCTGAGCGGTGTGGTGGTCACTGC 2049 Db 63GCTCAGCAATGGAGTATCCCAGTAAGCTAAGGAGAGTGC 13		Searon completed: May 25, 2005, 16:34:53 Job time : 1.87204 secs	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: May 25, 2005, 16:34:51 ; Search time 0.127959 Seconds (without alignments) 1.822 Million cell updates/sec</pre>	Title: US-10-005-337A-2_1715-2060	score:	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 0.0	Searched: 1 seqs, 337 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%

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O AGGGATGTGATCACCACCAAAGGAATGGCCTCTCACATTTCTTCTTGATTCACATATTC 119
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Compugen Ltd
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Maximum Match 100%
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                                                                      - nucleic search, using sw model
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 GenCore (c) 1993
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2358
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Result

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2224 CCCAGCCC - TAGCTATATAACGGCTGGT-GTGGAGG-GGCTCCACAGGGCCA-GTTCC 2278
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241 AAGATTATCTCACCCAGCCCTAGCTATAACGGGCTGGTGTGGAGGGCTCCACAGGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 CAGTGGCCAAT-TCAGAGGCAG----GTGAATTTTCATTCCAGACT--TAG--TGTCT-G 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GGAAĞCCCAAGAĞGGAGATGACAAGCTGGCCGCGTATGCGAATCAGGAAGAATGTG 95
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cive 0; Mismatches 107; Indels
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Copyright (c) 1993 - 2005 Compugen Ltd
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QUERY 1/c
T. Entered [bobryen 25-May-05 16:13]
QUERY_1
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Matches 170; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                           1 GCAATGTCAACAGACAGCTGTCCCCTGAC-TCTTGACAAATAGGATGACTTGCATTGCTG
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10.6%; Score 36.8; DB 1; Length 337;
Best Local Similarity 55.3%; Pred. No. 0;
Matches 146; Conservative 0; Mismatches 82; Indels 36;
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QUERY_1
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Search completed: May 25, 2005, 16:35:36 Job time : 1 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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- nucleic search, using sw model nucleic

Run on:

May 25, 2005, 16:36:21 ; Search time 0.872041 Seconds (without alignments) 1.822 Million cell updates/sec

US-10-005-337A-1-COPY 2358

Title: Perfect score:

1 ggatcctttcatgtttaaca.....caggtcggaggccaccatgg 2358 Sequence:

IDENTITY NUC Gapop $0.\overline{5}$, Gapext 0.0Scoring table:

Total number of hits satisfying chosen parameters:

1 segs, 337 residues

Searched:

seq length: 0 seq length: 2000000000 8 8 8 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

new.seg:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

QUERY_1 ; Entered [bobryen 25-May-05 16:13] QUERY_1

Gaps ö Length 337; 0; Indels 14.3%; Score 337; DB 1; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Query Match
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2031 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGGATGACTCGCATTGCTG 1972 GCAATATTAACAGGCAGCTGTCCCCTGGCTTCCCGATACGTGGGATGACTCGCATTGCTG g

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2212 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 2271 181 CACCTGCCTCTGAATTGGCCACTGGTGGGGGGCTGTGACTTGGCTTCCCAGGCTGG

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109; 241 AAGATTATCTCACCCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300 288 239 741 82 TICCTAGICTAGICCGITIGIGAAACICAGCCCAICCCAACACTICTGCAAGCCCCAICC 141 142 TCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCTTTCAGGATCAGCCTGATTCTA 201 314 202 GGGCAGCAGTICTCAACCTGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCCTTTAC 261 304 262 AGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAG 321 302 381 302 441 501 274 561 251 562 GAGCCAAGACGCATCGTGGGTGGAGCGAAGACGCAACCTCACCTTCTAGCTCTGCATCCA 621 681 232 801 207 861 22 TATCAACCCTAACCCAAGGGGAACAGCCTGCCTGACAGTGGCTTTGCCACCCATGAATAC 3.7 TAT-----------326 -----CTC-TTG-----TGGA------TGA-----TGA 442 ITCIGICCATICITCATICITCAAAGIGAIGIGITCACAGAAAGCCITICAGCIGITCIG 502 CTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTATGTACCAGGTCTGCTTCTTATGGGTG C----G---TTA-TA-----TAGGTG 622 TAGCAAGTAGCCTAATGTTTCTGTGTCTAGGTGTCATCTCTGTGAATCGAGATCCTTGGC 682 CTTGCTTGAATTAGGGAGGCACAAAATACTCAGAGATTCAAGACTGCTCAGCAGCCCCAGA 742 GICCTICCTCAAAGGAAAGGICTCAACTCTCAGCCCCCCTTAGCTCTGAGTCAGGCCTGG 302 AACAAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTGCTTGTCACTTCAAGAGGTCAA CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACAAT 301 --GGCC-----CTGT-----GGCC-----GG-AGCC-----CT------------GGAA------ACCCCT-----GGAA-----0; Indels 1973; DB 1; Length 337; 2272 CAGITCCAGGGTTCATCCACAAGAGAAAAACAIA 2308 301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 337 Query Match
12.0%; Score 282.5; Best Local Similarity 14.6%; Pred. No. 0; Matches 337; Conservative 0; Mismatches -----AGA-----T RESULT 2
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170	GGACAGATAGGACAGAGAGACCTAGGAGGGGGACCCACGAAGGACATATTAGT 981
982	GIGITGGITITCAGGGCAAIGICTIGIACTGAAGAITCIAGAAACACAAITIGCTGGTIG 1041
1042	AACAGCTGAAGTGGGGGGTTCTTACCCCATGTTCATGGAAGGTGAGTGA
1102	ACAGATATATGATGGCCAGCATAACAAACATACACAACACCCTAATTAACACTTCCCTCT 1161
1162	TCTACTGACACCCCCTTCACTCTTCATAAAAATAAAAAAGTATTTTATGG 1221
1222	
139	140
1282	TITIAATATCTTAGCGATGACAGGAAACAAGTATTTTTGCCTCTCTGAACAGCAA 1341 AGATGACAAGC
1342	AGCTIGGGGCCTTTTGTTTCCGTGTTAGGAATAGAACACGAGAGCCCCGTGTATCTAGG 1401
1402	CAGATGCTCTATCATTAGCCCATGAGTCTCCAGCCTCAGACGCACATTTTTCTCGGGCTC 1461
1462	TCTTAAGCTTTTCCCACAGCATTGGGAAACTTTACTGACAGCATCCAAGTTGTGCTTCTG 1521
1522	CTAAGAACTGGACTCACATCTCTGTGCATCACTTCGGCCCGTTTTGGGGTAGATCCTC 1581
1582	TGATTAGCCTTCAGATTTAGAACACGGGGGCCTGTGGTGCACTAATTATGGCCAGTGAC 1641 ATTCCTTTGG-CAGTGAC 70
1642	ACCATAGAGTCAAAGTGCATTACTGAATTTTCTCCTAATGCTGGTACGATGG 1701
1702	CATGICACAGGGCCATTTIAGCTGCAGACAICACTCCAGAGAATTCCAAACAGAIAGAGA 1761 CACA
1762	CAAGTGGCACCCAGACCCATCTCCCTCGGGCTGATTATCCCCCAGAAATAGGATGT 1821
1822	CCCAAAGCAACACTTCCCCAGCCAACTGGAGGGGTGTTAAGTCCAGTTATCAGAAAGATAT 1881
1882	GGCTGTAAGTGTGACACAGTGCTTGCATTTCTTGATACGTTAGTCATATGAGAGCTG 1941
1942	ACAAAGAAGGAAAAAAGAGCAGCGATGTGGTGCAATATTAACAGGCAGCTGTCCCCTGGCT 2001

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2122 ITCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGG 2181
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                                     2002 TCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACC 2061
                                                                                                                      2062 CICTCACATITCTTCCTGATICGCATACGCCGCCGCCAGCTIGTCATCTCCCTTTGGGC 2121
                                                                                                                                                                                                                                                                                       2182 GCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATA 2241
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1.822 Million cell updates/sec
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1 gcaatgtcaacagacagctg......cgacagaaaaacatacaaga 346
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                45 TCCC---ACGT-----AT-----CG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2302 AAACATAGACTCGAGGTCTAGGGAGCTTGC 2331
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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QUERY 1

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Query Match Length DB

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SUMMARIES

ALIGNMENTS

CGGTGTGGAGGGGC-CCAGCAGGCCAACTCCAGGGATTCCTTCCAC--GACAGAAAAAC 338 53 ATTGCTGAGCGATGTGATCAC--CACCAAAGGAATGGCCCTCTCACATTTCTTCCTGATT 110 54 ATTGCTGAGCGGTGTGGTCACTGC--CAAAGGAATGACCCTCTCACATTTCTTCCTGATT 111 111 CACATATTCAGCAG-GGTTAGCTTGTCCTCCCTCCCTTCAG--CTTCCCAGACACTG 167 AGTCTGGAATGAAAATTCACCTCTGAGTTGGCTC-CTAATGGGGGC-GGGAGTGTT 225 ACTTCGG-TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAA---GCTGAC 281 222 ACTT-GGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCTAGCTATATAACGGGCT--- 277 278 -Gereregaegegereca-caegeceaerrecaegeerr-carecaeaagagaaaaae 334 164 AGTCTGGAATGAAATTCACCTGCCTCTGAATTGGC-CACTGGTGGGGGCAGG-GTGTG 1 GCAATGTCAACAGACAGCTGTCCCCT-GACTCTT---GACAAATA----GGATGACTTGC Indels '48; Gaps Length 337; Query Match 75.9%; Score 262.5; DB 1; Best Local Similarity 79.9%; Pred. No. 0; Matches 290; Conservative 0; Mismatches 25; RESULT 1 QUERY 1 ; Entered (bobryen 25-May-05 16:13) QUERY 1 112 168 226 282 윰

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RESULT 2 QUERY 1/c : Entered [bobryen 25-May-05 16:13] QUERY_1 RESULT

ATA 341 ATA 337

207 TAAT---G-GGGGC-GG-GAGTGTT-----ACTICG-GT-T----CCC-AG-GT 241 86; 242 TGGAAGATTATCTCA-----CC-CGGCCCCAGCTATATAAGCTGA--CCGG-----TG 286 60 AGCGA--TG----TGATCACCACCAAAGGAATGGCCCTCT-CACATTCTTCCTGA---- 108 109 -TTCACATATTCAGC-AGGGTTAGCT---TGTCCTCCCTCCCTCCTTCAG-----CTTCC 158 272 GTT---ATAT--AGCTAGG----GCTGGGTG-------AGATAATCTT-C 240 CAGACACTGAGTCTGGAATG--AA---AATTCA--CCTGC-----CTCTGAGTTGGCTCC 206 336 Argrri------r-r-r-cr--crcris----r-scarcaacc---crc 307 306 ---chachecccrie-r-----eda---ecc-crecaca-----cc--accc 273 239 cag-c-crg-----ggaa-gccaagrca---cacccrgccccac-c--ag-rgg--cc 197 59 4 ATG--TCAACAGACAGCTGTCCCCTGACTCTTGACAAATAGGATGA--CTTGCATTGCTG 9; Indels 243; Gaps Query Match 46.1%; Score 159.6; DB 1; Length 337; Best Local Similarity 45.2%; Pred. No. 0; Matches 208; Conservative 0; Mismatches 9; Indels 243 159 g g ઠે g ò g δ ద Š

TG-GAGGGGC---CC---AGCAG-GGCCA-ACTC---CAG----G-GA-T--TCCTTCCA 326 96 TGAGAGGGTCATTCCTTTGGCAGTGACCACA-CGCTCAGCAATGCGAGTCATC---CCA 41 141 -GG-AGATGA----CAAGCTGGCCGCGC----G---TAT--GC-GAATCAGGAAGAAATG 97 327 CG-A-CAGAAA---A---ACA-----TACA-A--G 345 40 cerarceseaaccaseseacascascustra-ararre 2 287 셤 ઠે g ઠે g

Search completed: May 25, 2005, 16:36:23 Job time: 0.127959 secs

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                                                                                    May 25, 2005, 16:37:10 ; Search time 0.872041 Seconds (without alignments) 1.822 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGAGGGGCTCCACAGGGC 300
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                                                                                                                                                                                                                                                                                                                                             Gaps
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1.822 Million cell updates/sec
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                                                                                                                                                                                                                                                                                              Score 17.4; DB 1; Length 337;
Pred. No. 0;
                                                                                                                                                                                                                                                                                            cch 0.7%; Score 17.4; DB 1; Length 3:
al Similarity 53.7%; Pred. No. 0;
36; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                    2272 CAGTTCCAGGGGTTCATCCACAAGAGAAAAACATA 2308
                                                                                              301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAAACATA 337
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Maximum Match 100%
Listing first 45 summaries
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ne : 0.872041 secs
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                                                                                                                                                                                RESULT 2
QUERY 1/c
: Entered [bobryen 25-May-05 16:13]
QUERY_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGTGTGGGGGGCTCCAC 295
                                                                                                                                                                                                                                                         60 AGCGATGTGATCACCACCAAAGGAATGGCCCTCTCACATTTCTTCCTGATTCACATATTC 119
                                                                                                                                                                                                                                                                                                                                        120 AGCAGGGTTAGCTTGTCCTCCCTCCTTCTTCAGCTTCCCAGACACTGGGAATGA 179
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                                                                                                                                                                                                                    9
                                                                                                                                                                           6; Gaps
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49.0%; Score 169.6; DB 1; Length 337;
Best Local Similarity 75.1%; Pred. No. 0;
Matches 257; Conservative 0; Mismatches 79; Indels 6.
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RESULT 1
QUERY 1
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QUERY 1/c; ; Entered [bobryen 25-May-05 16:13] QUERY_1 GLEY_N MARKY

Query Match
3.7%; Score 12.8; DB 1; Length 337;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 29; Conservative 0; Mismatches 27; Indels 0;

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Search completed: May 25, 2005, 16:37:11 Job time : 0.127959 secs

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1589.292 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
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Gapop 60.0 , Gapext 0.0
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2358
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Entered [bobryen 25-May-05 16:13]
QUERY 1
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Maximum DB seq length: 200000000
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186 CAGGTGAATTTTCATTCCAGACTTAGTGTCTGGGAAGCCCAAGAGGGAGATGACAAGCTG 127
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53.7%; Pred. No. 0;
rative 0; Mismatches 31; Indels
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(c) 1993 - 2005 Compugen Ltd.
                                                                 2272 CAGTICCAGGGTICATCCACAAGAGAAAAAAAA 2308
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                 RESULT 2
QUERY 1/c
Fintered [bobryen 25-May-05 16:13]
QUERY_1
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                                                                                                              22 CCCCTGACTCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAG 81
                                                                                                                               Query Match 37.2%; Score 128.6; DB 1; Length 337; Best Local Similarity 73.8%; Pred. No. 0; Matches 236; Conservative 0; Mismatches 79; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    318 CCACAAGAGAAAAACATA 337
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Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels (RESULT 2 QUERY 1/c Fineered (bobryen 25-May-05 16:13) QUERY_1 à

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Search completed: May 25, 2005, 16:37:51 Job time : 0.001 secs

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1769 CACCCAG 1775
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Matches 36; Conserv
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                                                                                             May 25, 2005, 16:38:25 ; Search time 0.872041 Seconds (without alignments) 1.822 Million cell updates/sec
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                                                                                                                                                                                                 .....caggtcggaggccaccatgg 2358
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Compugen Ltd
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version 5
- 2005 (
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Maximum Match 100%
Listing first 45 summaries
                                                              - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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GenCore (c) 1993
                                                                                                                                                              US-10-005-337A-1-COPY
2358
                                                                                                                                                                                                                                                                               1 segs, 337 residues
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; Entered (bobryen 25-May-05 16:13)
QUERY_1
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Maximum DB seq length: 200000000
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337 1
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1709 CAGGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
241 AAGATTATCTCACCCAGCCCTAGCTATATAACGGGCTGGGTGTGGAGGGGCTCCACAGGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                           186 CAGGIGAATITITCATITCCAGACTIAGTGTCTGGGAAAGCCCAAGAGGGAGATGATGACAAGGTG 127
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1 gcaatgtcaacagacagctg......cgacagaaaaacatacaaga 346
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                           2272 CAGTTCCAGGGTTCATCCACAAGAGAAAAAAAAA 2308
                                                                                                   301 CAGTTCCAGGGGTTCATCCACAAGAGAAAAAACATA 337
                                                                                                                                                                                                                                                                                                           0.7%; Score 17.4; DB 1;
53.7%; Pred. No. 0;
tive 0; Mismatches 31;
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Maximum Match 100%
Listing first 45 summaries
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QUERY 1/c
Y Entered [bobryen 25-May-05 16:13]
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Match Length DB
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ALIGNMENTS

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                                                                                                                                                                    138 TCCCCTCCCTCTTCAGCTTCCCAGACACTGAGATGAAAATTCACCTGCCTCTGA 197
                                                                                                                                 258 CCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCCAGCAGCCCAACTCCAGGGA 317
                                                                                   0; Gaps
                                                       Query Match 34.9%; Score 120.8; DB 1; Length 337; Best Local Similarity 74.5%; Pred. No. 0; Matches 152; Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                    318 ITCCTTCCACGACAGAAAACATA 341
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RESULT 2

QUERY 1/c
; Entered [bobryen 25-May-05 16:13]

QUERY_1
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QUERY Match
3.7%; Score 12.8; DB 1; Length 337;
Best Local Similarity 51.8%; Pred. No. 0;
Matches 29; Conservative 0; Mismatches 27; Indels (

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0; Gaps

상 음 Search completed: May 25, 2005, 16:38:26 Job time : 0.127959 secs

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Score
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                                                                                                 May 25, 2005, 16:39:04 ; Search time 0.001 Seconds (without alignments) 1589.292 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
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337 1 QUERY 1
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2358
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QUERY 1
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QUERY_1
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length: 2000000000
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Match Length DB
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Maximum.DB seq
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1709 CAGGGCCATTTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGG 1768
186 CAGGIGAATITICATITCCAGACTIAGIGICTGGGAAAGCCCAAGAGGGGAGATGACAAGAGCTG 127
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346
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53.7%; Pred. No. 0;
tive 0; Mismatches 31; Indels
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                      2272 CAGTTCCAGGGTTCATCCACAGAGAGAAAAACATA 2308
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Maximum Match 100%
Listing first 45 summaries
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time : 1 secs
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                                                                                                                                                                                RESULT 2
QUERY 1/c
Y. Entered [bobryen 25-May-05 16:13]
QUERY_1
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Maximum DB seq length: 200000000
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337 1
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Match Length DB
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.73
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                new.sed:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1769 CACCCAG 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 GCCGCGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.9
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ALIGNMENTS

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                                                                                                                                                                      138 TCCCTCCTCTTCAGCTTCCCAGACACTGAGATGAAAATTCACCTGCCTCTGA 197
                                                                                                                                                                                                                                                                      194 ATTGGCCACTGGTGGGGGCAGGGGTGTGACTTCCCAGGCTGGAAGATATCTCAC 253
                                                                                                                                                                                                                                                                                                                           258 CCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGGCCCCAGCAGGCCCAACTCCAGGGA 317
                                                                                                                                                                                                                                                                                                                                                  134 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGA 193
                                                                                                                                                                                                                                                198 GTTGGCTCCTAATGGGGGGGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCAC 257
                                                                                                                                     0; Gaps
                                                                                            Score 120.8; DB 1; Length 337;
Pred. No. 0;
0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                   318 TTCCTTCCACGACAGAAAACATA 341
                                                                                                                                                                                                                                                                                                                                                                                                                           314 TCATCCACAAGAGAGAAAAACATA 337
RESULT 1
QUERY 1
Fintered [bobryen 25-May-05 16:13]
QUERY_1
                                                                                              Query Match
Best Local Similarity 74.5%;
Matches 152; Conservative
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Query Match 3.7%; Score 12.8; DB 1; Length 337; Best Local Similarity 51.8%; Pred. No. 0; Matches 29; Conservative 0; Mismatches 27; Indels RESULT 2 QUERY 1/c ; Entered (bobryen 25-May-05 16:13) QUERY_1

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0; Gaps

Search completed: May 25, 2005, 16:39:05 Job time : 0.001 secs